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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/029,890

DATE: 04/16/2002
TIME: 16:08:03

Input Set : N:\Crf3\RULE60\10029890.raw
Output Set: N:\CRF3\04162002\J029890.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
 4 (i) APPLICANT: Soos, Jeanne M.
 5 Schiffenbauer, Joel
 6 Johnson, Howard M.
 8 (ii) TITLE OF INVENTION: Orally-Administered Interferon-Tau
 9 Compositions and Methods
 11 (iii) NUMBER OF SEQUENCES: 6
 13 (iv) CORRESPONDENCE ADDRESS:
 14 (A) ADDRESSEE: Dehlinger & Associates
 15 (B) STREET: 350 Cambridge Ave., Suite 250
 16 (C) CITY: Palo Alto
 17 (D) STATE: CA
 18 (E) COUNTRY: USA
 19 (F) ZIP: 94306
 21 (v) COMPUTER READABLE FORM:
 22 (A) MEDIUM TYPE: Floppy disk
 23 (B) COMPUTER: IBM PC compatible
 24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
 27 (vi) CURRENT APPLICATION DATA:
 C--> 28 (A) APPLICATION NUMBER: US/10/029,890
 C--> 29 (B) FILING DATE: 21-Dec-2001
 30 (C) CLASSIFICATION:
 33 (vii) PRIOR APPLICATION DATA:
 34 (A) APPLICATION NUMBER: US/08/616,904
 35 (B) FILING DATE: 15-MAR-1996
 38 (viii) ATTORNEY/AGENT INFORMATION:
 39 (A) NAME: Sholtz, Charles K.
 40 (B) REGISTRATION NUMBER: 38,615
 41 (C) REFERENCE/DOCKET NUMBER: 5600-0003
 43 (ix) TELECOMMUNICATION INFORMATION:
 44 (A) TELEPHONE: 415-324-0880
 45 (B) TELEFAX: 415-324-0960
 47 (2) INFORMATION FOR SEQ ID NO: 1:
 49 (i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 516 base pairs
 51 (B) TYPE: nucleic acid
 52 (C) STRANDEDNESS: double
 53 (D) TOPOLOGY: circular
 W--> 55 (ii) MOLECULE TYPE: DNA
 57 (iii) HYPOTHETICAL: NO
 W--> 85 (iv) ANTI-SENSE: Purification and Antiviral Activity

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Input Set : N:\Crf3\RULE60\10029890.raw
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61 (vi) ORIGINAL SOURCE:
 62 (A) ORGANISM: Ovis aries
 63 (B) STRAIN: Domestic
 64 (D) DEVELOPMENTAL STAGE: Blastula (blastocyst)
 65 (F) TISSUE TYPE: Trophectoderm
 66 (G) CELL TYPE: Mononuclear trophectoderm cells
 68 (vii) IMMEDIATE SOURCE:
 C--> 82 (B) CLONE: Cloning and Expression in *Saccharomyces*
 83 cerevisiae of a Synthetic Gene for the Type I
 84 Trophoblast Interferon Ovine Trophoblast
 71 (viii) POSITION IN GENOME:
 72 (C) UNITS: bp
 74 (ix) FEATURE:
 75 (A) NAME/KEY: CDS
 76 (B) LOCATION: 1..516
 77 (x) PUBLICATION INFORMATION:
 78 (A) AUTHORS: Ott, Troy L
 79 Van Heeke, Gino
 80 Johnson, Howard M
 81 Bazer, Fuller W
 92 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 94 TGC TAC CTG TCG CGA AAA CTG ATG CTG GAC GCT CGA GAA AAT TTA AAA 48
 95 Cys Tyr Leu Ser Arg Lys Leu Met Leu Asp Ala Arg Glu Asn Leu Lys
 96 1 5 10 15
 98 CTG CTG GAC CGT ATG AAT CGA TTG TCT CCG CAC AGC TGC CTG CAA GAC 96
 99 Leu Leu Asp Arg Met Asn Arg Leu Ser Pro His Ser Cys Leu Gln Asp
 100 20 25 30
 102 CGG AAA GAC TTC GGT CTG CCG CAG GAA ATG GTT GAA GGT GAC CAA CTG 144
 103 Arg Lys Asp Phe Gly Leu Pro Gln Glu Met Val Glu Gly Asp Gln Leu
 104 35 40 45
 106 CAA AAA GAC CAA GCT TTC CCG GTA CTG TAT GAA ATG CTG CAG CAG TCT 192
 107 Gln Lys Asp Gln Ala Phe Pro Val Leu Tyr Glu Met Leu Gln Gln Ser
 108 50 55 60
 110 TTC AAC CTG TTC TAC ACT GAA CAT TCT TCG GCC GCT TGG GAC ACT ACT 240
 111 Phe Asn Leu Phe Tyr Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr
 112 65 70 75 80
 114 CTT CTA GAA CAA CTG TGC ACT GGT CTG CAA CAG CAA CTG GAC CAT CTG 288
 115 Leu Leu Glu Gln Leu Cys Thr Gly Leu Gln Gln Leu Asp His Leu
 116 85 90 95
 118 GAC ACT TGC CGT GGC CAG GTT ATG GGT GAA GAA GAC TCT GAA CTG GGT 336
 119 Asp Thr Cys Arg Gly Gln Val Met Gly Glu Glu Asp Ser Glu Leu Gly
 120 100 105 110
 122 AAC ATG GAT CCG ATC GTT ACT GTT AAA AAA TAT TTC CAG GGT ATC TAC 384
 123 Asn Met Asp Pro Ile Val Thr Val Lys Lys Tyr Phe Gln Gly Ile Tyr
 124 115 120 125
 126 GAC TAC CTG CAG GAA AAA GGT TAC TCT GAC TGC GCT TGG GAA ATC GTA 432
 127 Asp Tyr Leu Gln Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Ile Val
 128 130 135 140
 130 CGC GTT GAA ATG ATG CGG GCC CTG ACT GTG TCG ACT ACT CTG CAA AAA 480

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131 Arg Val Glu Met Met Arg Ala Leu Thr Val Ser Thr Thr Leu Gln Lys
 132 145 150 155 160
 134 CGG TTA ACT AAA ATG GGT GGT GAC CTG AAT TCT CCG
 135 Arg Leu Thr Lys Met Gly Gly Asp Leu Asn Ser Pro
 136 165 170

516

138 (2) INFORMATION FOR SEQ ID NO: 2:

140 (i) SEQUENCE CHARACTERISTICS:
 141 (A) LENGTH: 172 amino acids
 142 (B) TYPE: amino acid
 143 (D) TOPOLOGY: linear
 145 (ii) MOLECULE TYPE: protein
 147 (vi) ORIGINAL SOURCE:

148 (C) INDIVIDUAL ISOLATE: amino acid sequence of a mature
 149 OvIFNtau protein

151 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

153 Cys Tyr Leu Ser Arg Lys Leu Met Leu Asp Ala Arg Glu Asn Leu Lys
 154 1. 5 10 15

156 Leu Leu Asp Arg Met Asn Arg Leu Ser Pro His Ser Cys Leu Gln Asp
 157 20 25 30

159 Arg Lys Asp Phe Gly Leu Pro Gln Glu Met Val Glu Gly Asp Gln Leu
 160 35 40 45

162 Gln Lys Asp Gln Ala Phe Pro Val Leu Tyr Glu Met Leu Gln Gln Ser
 163 50 55 60

165 Phe Asn Leu Phe Tyr Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr
 166 65 70 75 80

168 Leu Leu Glu Gln Leu Cys Thr Gly Leu Gln Gln Leu Asp His Leu
 169 85 90 95

171 Asp Thr Cys Arg Gly Gln Val Met Gly Glu Glu Asp Ser Glu Leu Gly
 172 100 105 110

174 Asn Met Asp Pro Ile Val Thr Val Lys Lys Tyr Phe Gln Gly Ile Tyr
 175 115 120 125

177 Asp Tyr Leu Gln Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Ile Val
 178 130 135 140

180 Arg Val Glu Met Met Arg Ala Leu Thr Val Ser Thr Thr Leu Gln Lys
 181 145 150 155 160

183 Arg Leu Thr Lys Met Gly Gly Asp Leu Asn Ser Pro
 184 165 170

187 (2) INFORMATION FOR SEQ ID NO: 3:

189 (i) SEQUENCE CHARACTERISTICS:
 190 (A) LENGTH: 516 base pairs
 191 (B) TYPE: nucleic acid
 192 (C) STRANDEDNESS: single
 193 (D) TOPOLOGY: linear
 195 (ii) MOLECULE TYPE: cDNA
 197 (vi) ORIGINAL SOURCE:

198 (C) INDIVIDUAL ISOLATE: synthetic nucleotide sequence encoding
 199 a mature human interferon-tau protein, HuIFNtau1.

201 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

203 TGTGACTTGT CTCAAAACCA CGTTTGGTT GGTAGAAAGA ACTTAAGACT ACTAGACGAA

60

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205 ATGAGACGTC TATCTCCACG CTTCTGTCTA CAAGACAGAA AGGACTTCGC TTTGCCTCAG 120
207 GAAATGGTTG AAGGTGGCCA ACTACAAGAA GCTCAAGCGA TATCTGTTTT GCACGAAATG 180
209 TTGCAACAAA GCTTCAACATT GTTCCACACC GAACACTCTT CGGCCGCTTG GGACACCAACC 240
211 TTGTTGGAAC AGCTCAGAAC CGGTTTGAC CAACAATTGG ACAACTTGGA TGCATGTTG 300
213 GGTCAAGTTA TGGGTGAAGA AGACTCTGCT CTCGGGAGAA CGGGTCCAAC GCTAGCTTTG 360
215 AAGAGATACT TCCAAGGTAT CCACGTTAC TTGAAGGAAA AGGGTTACTC TGACTGTGCT 420
217 TGGGAAACCG TGCCTCTAGA ATCATGCGT AGCTTCTCTT CTTTGATCAG CTTGCAAGAA 480
219 AGATTACGTA TGATGGACGG TGACTTGTGAGGCCA 516

221 (2) INFORMATION FOR SEQ ID NO: 4:

223 (i) SEQUENCE CHARACTERISTICS:
224 (A) LENGTH: 172 amino acids
225 (B) TYPE: amino acid
226 (C) STRANDEDNESS: single
227 (D) TOPOLOGY: linear

229 (ii) MOLECULE TYPE: protein

231 (vi) ORIGINAL SOURCE:
232 (C) INDIVIDUAL ISOLATE: amino acid sequence for a mature
233 HuIFNtau protein, HuIFNtau1.

235 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

237 Cys Asp Leu Ser Gln Asn His Val Leu Val Gly Arg Lys Asn Leu Arg
238 1 5 10 15
240 Leu Leu Asp Glu Met Arg Arg Leu Ser Pro Arg Phe Cys Leu Gln Asp
241 20 25 30
243 Arg Lys Asp Phe Ala Leu Pro Gln Glu Met Val Glu Gly Gly Gln Leu
244 35 40 45
246 Gln Glu Ala Gln Ala Ile Ser Val Leu His Glu Met Leu Gln Gln Ser
247 50 55 60
249 Phe Asn Leu Phe His Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr
250 65 70 75 80
252 Leu Leu Glu Gln Leu Arg Thr Gly Leu His Gln Gln Leu Asp Asn Leu
253 85 90 95
255 Asp Ala Cys Leu Gly Gln Val Met Gly Glu Glu Asp Ser Ala Leu Gly
256 100 105 110
258 Arg Thr Gly Pro Thr Leu Ala Leu Lys Arg Tyr Phe Gln Gly Ile His
259 115 120 125
261 Val Tyr Leu Lys Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Thr Val
262 130 135 140
264 Arg Leu Glu Ile Met Arg Ser Phe Ser Ser Leu Ile Ser Leu Gln Glu
265 145 150 155 160
267 Arg Leu Arg Met Met Asp Gly Asp Leu Ser Ser Pro
268 165 170

270 (2) INFORMATION FOR SEQ ID NO: 5:

272 (i) SEQUENCE CHARACTERISTICS:
273 (A) LENGTH: 516 base pairs
274 (B) TYPE: nucleic acid
275 (C) STRANDEDNESS: double
276 (D) TOPOLOGY: linear
278 (ii) MOLECULE TYPE: DNA (genomic)
280 (iii) HYPOTHETICAL: NO

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Input Set : N:\Crf3\RULE60\10029890.raw
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282 (iv) ANTI-SENSE: NO
284 (vi) ORIGINAL SOURCE:
285 (C) INDIVIDUAL ISOLATE: HuIFNtau3, mature no leader sequence
287 (ix) FEATURE:
288 (A) NAME/KEY: CDS
289 (B) LOCATION: 1..516
291 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
293 TGT GAC CTG TCT CAG AAC CAC GTG CTG GTT GGC AGC CAG AAC CTC AGG 48
294 Cys Asp Leu Ser Gln Asn His Val Leu Val Gly Ser Gln Asn Leu Arg
295 1 5 10 15
297 CTC CTG GGC CAA ATG AGG AGA CTC TCC CTT CGC TTC TGT CTG CAG GAC 96
298 Leu Leu Gly Gln Met Arg Arg Leu Ser Leu Arg Phe Cys Leu Gln Asp
299 20 25 30
301 AGA AAA GAC TTC GCT TTC CCC CAG GAG ATG GTG GAG GGT GGC CAG CTC 144
302 Arg Lys Asp Phe Ala Phe Pro Gln Glu Met Val Glu Gly Gly Gln Leu
303 35 40 45
305 CAG GAG GCC CAG GCC ATC TCT GTG CTC CAC GAG ATG CTC CAG CAG AGC 192
306 Gln Glu Ala Gln Ala Ile Ser Val Leu His Glu Met Leu Gln Gln Ser
307 50 55 60
309 TTC AAC CTC TTC CAC ACA GAG CAC TCC TCT GCT GCC TGG GAC ACC ACC 240
310 Phe Asn Leu Phe His Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr
311 65 70 75 80
313 CTC CTG GAG CAG CTC CGC ACT GGA CTC CAT CAG CAG CTG GAT GAC CTG 288
314 Leu Leu Glu Gln Leu Arg Thr Gly Leu His Gln Gln Leu Asp Asp Leu
315 85 90 95
317 GAT GCC TGC CTG GGG CAG GTG ACG GGA GAG GAA GAC TCT GCC CTG GGA 336
318 Asp Ala Cys Leu Gly Gln Val Thr Gly Glu Glu Asp Ser Ala Leu Gly
319 100 105 110
321 AGA ACG GGC CCC ACC CTG GCC ATG AAG AGG TAT TTC CAG GGC ATC CAT 384
322 Arg Thr Gly Pro Thr Leu Ala Met Lys Arg Tyr Phe Gln Gly Ile His
323 115 120 125
325 GTC TAC CTG AAA GAG AAG GGA TAT AGT GAC TGC GCC TGG GAA ATT GTC 432
326 Val Tyr Leu Lys Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Ile Val
327 130 135 140
329 AGA CTG GAA ATC ATG AGA TCC TTG TCT TCA TCA ACC AGC TTG CAC AAA 480
330 Arg Leu Glu Ile Met Arg Ser Leu Ser Ser Thr Ser Leu His Lys
331 145 150 155 160
333 AGG TTA AGA ATG ATG GAT GGA GAC CTG AGC TCA CCT 516
334 Arg Leu Arg Met Met Asp Gly Asp Leu Ser Ser Pro
335 165 170
338 (2) INFORMATION FOR SEQ ID NO: 6:
340 (i) SEQUENCE CHARACTERISTICS:
341 (A) LENGTH: 172 amino acids
342 (B) TYPE: amino acid
343 (D) TOPOLOGY: linear
345 (ii) MOLECULE TYPE: protein
347 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
349 Cys Asp Leu Ser Gln Asn His Val Leu Val Gly Ser Gln Asn Leu Arg
350 1 5 10 15

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/029,890

DATE: 04/16/2002

TIME: 16:08:04

Input Set : N:\Crf3\RULE60\10029890.raw

Output Set: N:\CRF3\04162002\J029890.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:82 M:220 C: Keyword misspelled or invalid format, [(B) CLONE:]
L:85 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:55 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1
L:85 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=1